SYNOPSIS OF RESEARCH PROJECT

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4.	**Name of the Degree Submitted for**	**:**	Ph.D. (Agri.)
5.	**Major Subject**	**:**	Agricultural Statistics
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8.	**Title of Research Problem**	**:**	**"A Comparative Study of Statistical Approaches for Genotype × Environment Interaction and Stability Analysis in Irrigated Chickpea (*Cicer arietinum* L.) Crop"**

9. Introduction

Chickpea (*Cicer arietinum* L.) is a most significant pulse crop in India with ranked first which contributes 43% of total pulse production. chickpea is grown on about 9.61 million ha producing 11.34 million tons of seed with productivity of 1180 kg/ha in 2024-25 in India, while in Gujarat state, area under chickpea was 8.50 lakh hac with a production of 15.64 lakh tonnes and productivity of 1841 kg/ha during 2024-25. Chickpea has become more important to mitigate the problem of protein energy malnutrition. Aside from being an excellent source of highly digestible dietary protein (18-22%). It is also highly rich in calcium, iron, niacin, vitamins B, and C. It gives 396 kcal of energy per 100 grams of seed.

One of the biggest challenges facing crop improvement initiatives is the effect of Genotype × Environment interaction (GEI), which may be defined as performance of different genotypes in different environments. This implies that due to the effect of G × E interaction, a genotype that gives good performance in a particular environment may not give similar performance in another environment. This interaction effect, therefore, poses a challenge in the search for a more stable and high-yielding genotype,

which calls for evaluation of genotypes in different environments through multi-location trial (MLT).

The genotypes have to have the genetic ability to show superior performance under ideal environments, as well as the ability to show acceptable performance under less-than-ideal environments. A stable genotype could thus be described as the one which has the ability to use the available resources in the high yield environment, as well as the ability to show a mean performance which is above average in all environments as per (Eberhart & Russell, 1966).

A breeder's understanding of the genotype-environment interaction (GEI) is critical for developing new varieties. In a plant breeding effort, multiple possible genotypes are often examined in different environments before being chosen. The G x E interaction has a masking effect on the genotype's performance, and thus the relative ranking of the genotypes does not remain constant across the number of environments for quantitative traits such as seed yield; the relative performance of the different genotypes varies from one environment to the next, indicating that G x E interaction exists. The shift in ranking makes it difficult for the plant breeder to choose which genotype to use.

Yield is a complex quantitative characteristic which is influenced by large number of genes that is determined by both genotype and agroclimatic environment. It is a reality that a phenotypic performance of genotype may vary depending on the environment and that not all genotypes will exhibit phenotypic performance at the same level. On the other hand, Agronomically, Stability has been defined as the buffering capacity of genotypes to environmental fluctuations in order to demonstrate the uniform development of the crop and crop yield. Genetically, stability refers to the ability of a genotype to remain consistent in a wide range of environmental conditions. The stability of the genotypes in relation to the changing environment has always remained a major concern to the plant breeders. Several statistics have been proposed in the past to evaluate the phenotypic stability of various genotypes in a changing environment. In the chickpea breeding program, it is critical to identify phenotypically stable genotypes that can perform consistently in different environments.

Many of the statistical tools for stability analysis have been developed to address the complexity of G × E interactions. In the past, parametric techniques like variance component approaches and regression-based models have been extensively utilized. Certain statistical characteristics, including homogeneity of variance and

normality, are assumed by these techniques. The Additive Main Effects and Multiplicative Interaction (AMMI) model has become increasingly important because it combines principal component analysis (PCA) for interaction effects with analysis of variance (ANOVA) for additive effects. A strong foundation for interpreting G × E interaction patterns and identifying stable genotypes across environments is offered by the AMMI model. Various Modified AMMI models have been proposed in recent years to improve genotype stability analysis accuracy. The decomposition of interactions, stability evaluation and genotype ranking are all improved in these Modified AMMI models, which may be useful in identifying the genotype in a complex agricultural scenario where the impact of the environment on crop yield cannot be neglected.

The advanced statistical methodology utilized in plant breeding is the Best Linear Unbiased Prediction (BLUP). BLUP is a mixed effect based approach for genotype performance prediction. When making predictions, it takes both random and fixed effects into account. By utilizing data from all contexts and variance components, BLUP estimates genotype performance more accurately than traditional techniques. In multi-environment experiments, BLUP has become an effective method to find high-performing genotypes.

Besides the parametric approach, non-parametric approaches to stability analysis have drawn attention in last decades. Non-parametric techniques are considered to be reliable to check the stability of genotypes where statistical assumptions underlying parametric techniques are not fulfilled as it is based on ranking of genotypes in different environments. The integration of parametric and non-parametric approaches for assessing genotypic stability with models such as Modified AMMI and BLUP is essential for understanding genotypes in depth. This type of study can help select stable and high-yielding genotypes for chickpea farming in various agro-climatic areas.

10. Practical Utility of the Research Project

The proposed research will provide significant benefits for the crop improvement and statistical evaluation of chickpea (*Cicer arietinum* L.). With the use of genotype × environment interaction, Modified AMMI and BLUP models, it will be feasible to find stable and high-yielding genotypes of the crop across different environments. In the addition, the research will compare various statistical parametric and non-parametric stability analysis techniques to determine their effectiveness for assessing genotype stability and adaptability. Researchers and plant breeders will be able to determine the

most appropriate statistical techniques in multi-environment trial analysis. The findings of the study will strengthen pulse production in India by supporting the development and recommendation of stable chickpea varieties and contributes to improved decision making in breeding programmes. Considering this, the present study is undertaken with the given objectives:

11. Objectives

1. To assess GEI magnitude for seed yield in irrigated chickpea genotypes.
2. To find out the stable genotype of irrigated chickpea crop.
3. To study univariate, multivariate and regression methods of stability analysis.
4. To asses effect of fixed and random effect models of stability analysis.
5. To compare various methods of stability analysis using rank correlation.

12. Review of Literature

Pulses hold a significant position in the agrarian economy of our country. This superior source of protein-rich nutrients for millions of people is vital to both intensive and subsistence farming. The production of chickpeas contributed to 48% of India's total pulse production, followed by pigeon peas 15%, mungbeans 7%, urdbeans 7%, lentils 5%, and field peas 5%. This chapter deals with reviews of related past studies. Keeping in view of the objective of the study, the reviews has been written in following headings:

12.1 Genotype-Environment Interaction (G EI)

12.2 Stability analysis

12.2.1 Parametric models

12.2.2 Nonparametric models

12.2.3 Regression models

12.2.4 Multivariate models

12.2.5 Effect of fixed and random effect model

12.3 Comparison of different stability models

12.1 Genotype-Environment Interaction (GEI)

Singh and Choudhary (1984) assessed 32 genotypes in three different habitats; genotypes that demonstrated stability in both favorable and unfavorable conditions were found.

Mishra *et al.* (1999) examined the effects of GE interaction on six yield-related variables in 20 genotypes of rainfed soybeans grown between 1993 and 1997. There were notable interactions between the environment and genotype. With the exception of pods/plant, all characters showed a substantial linear component of GEI. For every character among the 20 genotypes examined, the non-linear component was significant.

Deka and Talukdar (1997) investigated the stable behavior of 21 soybean germplasm.for yield and some of the yield attributable under five distinct conditions. Nearly every character showed a significant GE interaction; both linear and nonlinear components contributed to the variance of the GE interaction. The genotypes Moti, PK-80, PK-472, BD-1, BD-12, Bragg, and PK-73-203 demonstrated mean seed yield stability and the stability of Ds-16-1-37-1 was above average.

Roy and Roquib (1998) used twenty improved soybean cultivars that were grown in India during the 1993 kharif season or the 1993–1994 rabi season. The cultivars with the highest kharif yields were JS 80-21, Bragg, PK-482, Durga , in decreasing order. In Rabi, the cultivars PK-262, Punjab-1, Pusa-16, PK411, and JS 75-46 had the highest yields.

Rawat et al. (2001) found that the mean square for the genotype x environment interaction was significant for all 60 genotypes with the exception of seedling development rate,. In every habitat, the most stable genotypes for germination rate were the most consistent seedling growth rates across all conditions. Overall, JS 72-280, JS 81, JS 76-205, JS 80-21, -1619, JS 87-60 and Ankur were the most stable genotypes.

Joshi et al. (2005) discovered substantial variations between genotypes, environments (locations), and genotype x environment interactions. Only the non-linear component of G x E interactions was significant for days to 50% flowering and days to maturity for each variable,, although both the linear and non-linear components were significant for plant height, 100-seed weight, and seed yield. Three genotypes—J-793, SL-87, and JS-335—were found to be stable for seed yield.

Sudaric et al. (2005) observed significant differences in the degree and stability of grain production, grain quality, and genotype adaptation .Three groups of additional genotypes were identified: stable genotypes with broad general adaptability, unstable genotypes adapted to high-yielding situations, and unstable genotypes adapted to low-yielding conditions of the thirty-two genotypes that were evaluated, twenty were stable for protein content, seventeen were consistent for grain oil content, and twenty-two were stable for grain yield.

Mahajan *et al.* (2006) examined soybean lines over time at mid-altitudes in the northwest Himalayas. Yield, plant height, days to blooming, and maturity were found to be significantly influenced by genotypes, years, and their interaction. While VS 2173 and VS 2174 were stable, dwarf, and on level with VLS 47 in terms of yield and other characteristics, VL 2157 and VS 495 were superior for yield over VLS 47 and sensitive to the better conditions. Thus, it was determined that VL 2157, VS 495, and VS 2173 were promising and could be investigated in a variety of settings under the national soybean program.

Lodhi *et al.* (2015) examined 105 barley genotypes' stability performance in three distinct settings using a randomized block design and three replicates. They demonstrated that interactions between genotype and environment were extremely important for every character under investigation. Additionally, they showed that the genotypes Manjula and EIBGN-04-14 for the grains per ear and EIBGN-2-1 and Jyoti for the grain production per plant were found to be very stable across the conditions. In a program to develop barley for target environments, these promising genotypes might be used as donors.

12.2 Stability analysis

12.2.1 Parametric models

Dias and Krzanowski (2006) evaluated wheat genotypes in 20 locations using nine cultivars. They selected the number of multiplicative interaction components using four distinct approaches, which showed varying outcomes on the simulated data sets. The four approaches exhibit various behavioural tendencies. The Eastment-Krzanowski approach, which selects a m value of 2 for the original data as opposed to 1 or 2 for all simulations, is incredibly stable.

Parmar *et al.* (2012) investigated yield data pertaining to 21 rice varieties' responsiveness to changing soil and climate conditions. GEI were found to be highly significant in the combined or pooled ANOVA results. Genetic diversity among genotype yield was indicated by significant genotypic variance. The genotypes IET-19147, NWGR-3006, NWGR-3006, IET-19123, and IET-19147 were shown to be stable.

Wricke (1962) proposed ecovalence (Wi2) as a measure of the stability of the ith genotype by calculating the contribution of each genotype to the GEI sum of squares. Ecovalence is zero in stable genotypes (high ecovalence indicates low stability).

Shukla (1972) defined the stability variance genotype "i" as the variance (σi2) in the environments after correcting for environmental mean main effects. In a two-way classification, the stability variance is based on the residual (GEij+eij) matrix, with stable varieties having smaller estimates.

Francis and Kannenberg (1978) investigated the yield stability of 15 genotypes of short-season maize that were grown between 1969 and 1974 in 16 different locations in Southern Ontario. They proposed classifying genotypes based on maize yield and C.V. using Mean and C.V. as stability parameters. Genotype means yield was plotted against C.V. Mean C.V. and grand mean yield split the graph into four groups: Group I: little variation and high yield; Group II: large variation and high yield; Group III: small variation and low yield; and Group IV: huge variation and low yield.The genotypes in the first of the four groups had a high mean yield and little variation, while those in the second group had a high yield and significant variation. The fourth group had a low yield and significant variation, while the third group had a low yield and little variation.

12.2.2 Nonparametric models

Nassar and Huehn (1987) examined on 20 genotypes (varieties) of winter wheat tested in ten settings (environmets) in Germany using nonparametric measures of stability. The results indicated that, with the exception of JUBILAR and F, which were significant, there was no proof that the differences in stability among the 20 variants. They came to the conclusion that Jubilar and F's relevance might be random. The global test shows no appreciable variation in stability and is more dependable.

Huehn (1990) used data on winter wheat grain yield from registration trials carried out in Germany between 1974 and 1976 to develop three non-parametric stability parameters viz. Si1, Si2, and Si3 and compared them with the classical stability parameters. The analysis revealed that there was variation in both the magnitude and sign of the connection between the non-parametric parameters and the traditional stability parameters. While there was a moderately favorable association between the non-parametric parameters and ecovalence and regression deviation, there was very little link between the non-parametric parameters and the regression coefficient and environmental variance. The association changed over time.

Vieiral *et al.* (2006) examined the average performance of cultivars in six conditions, both with and without fungicide application, using nonparametric selection indicators. The indices used in this study were the classification sum index, modified classification sum index (using the standard deviation in the separation of means), and index of distance to the ideotype. Cultivar UPFA22 was identified as the best genotype across all criteria, making it stand out. Additionally, the cultivar's hectoliter weight and grain yield were well-classified.

Akcura and Kaya (2008) have stated that assessing high yield and performance stability is crucial for yield studies carried out in various settings. Using nonparametric stability metrics, They examined nonparametric stability statistics in 19 locations in the Central Anatolian Region of Turkey and evaluated the stability of 10 genotypes of bread wheat (Triticum aestivum L.), including five cultivars and five advanced lines. Nonparametric stability measurements showed that AL-2, Karahan-99, and Altay-2000 were the most stable and well-adapted genotypes in all 19 situations. Additionally, it was discovered that the visual efficacy of genotype selection based on genotype by environment interaction was enhanced by graphs of mean grain yield (t ha-1) vs. nonparametric metrics (Si (1), Si (2), Si (3), Si (6), and gy) values and kr vs. r values.

Delic *et al.* (2009) have analyzed the GE interaction for grain yield of 24 hybrids of maize in two locations over a two-year period using non-parametric methods. The majority of the time, hybrids with the highest grain production were not the most stable, according to the stability measure values. The lowest yield genotype PR36B08 was therefore identified as the stable genotype (Si (3) = 0.12) based on the value of the deviation in reference to the mean rank.

Zekimut *et al.* (2009) discovered potential high-yield and stable bread wheat genotypes in seven locations in the central Black Sea region of Turkey between 2003 and 2005 By comparing nonparametric stability indices. To find stable genotypes in seven contexts, ten nonparametric methods of stability and three nonparametric test of significance for GEI were employed. The most stable genotypes for grain yield were G7 (VONA), G9 (JUP/4/CLLF), G20 (Sakin), and G21 (VORONA) based on these stability measures (TOP and rank-sum).

12.2.3 Regression models

Yates and Cochran (1938) suggested joint regression analysis as a way to examine the linear responses of genotypes to various environments.

Eberhart and Russell (1966) enhanced the Finlay and Wilkinson model in order to characterize the performance of variety over time and space and proposed three stability parameters: means, regression coefficients (bi), and departure from linearity (S2di). Additionally, they recommended that while evaluating the genotype's phenotypic stability, both linear and non-linear functions be taken into account.

Hanson (1970) utilized smallest slope as one of the criteria from the Eberhart and Russell analysis. The deviation of a predicted yield from the yield Based on their coordinate coordinates, the genotypes are categorized if the genotype was stable.

Kabir *et al.* (2009) have studied GEI for various wheat genotypes in eight different planting dates over two years in Bangladesh under irrigated conditions using a rbd design with three replicates. To determine the ideal sowing date, they also employed the Eberhart and Russell Stability method of linear regression.as per research, November 29 was the ideal day to grow wheat in Bangladesh.

12.2.4 Multivariate models

Gabriel (1971) developed the biplot concept using principal components analysis. A helpful data analysis tool that enables the visual examination of a huge data matrix's structure is the biplot. Along with the variances and correlations of the variables, it displays the units' distance and clustering.

Mohammadi *et al.* (2012) carried out a study utilizing the GGE biplot technique to analyze genotype, environment, and GEI with 18 bread wheat genotypes under multi-environment circumstances in warm rain-fed districts of Iran. The findings demonstrated that both main effects (genotype and environment) and GEI were very

significant when combined analysis of variance across nine locations was carried out. In order to generate a GGE biplot diagram, they also employed principal component analysis. Major two components are explaining maximum variation as 45% and 26% of the total sum of squares. Furthermore, G1 and G4 were the most stable genotypes in Iran's warm, rain-fed region, according to GGE Biplot data.

Goa and Mohammad (2013) have assessed GEI and yield stability at five environments in Southern Ethiopia using twenty-four field peas. Genotypes between 2006 and 2007. Using the ANOVA test, they demonstrated that yield and its yield-related variables, the major effects resulting from genotype, locations, and the genotype x location were very significant. Additionally, they employed a few parametric measurements, and it was discovered that there was a highly substantial association between yield and these parametric measures. The best stable genotype was found using the AMMI approach, and "IG-51980" was found to be the most desirable and appropriate genotype that demonstrated consistent yields and was suggested for commercial cultivation in south Ethiopia.

Tolessa et al. (2013) investigated 14 field pea genotypes in 16 environments throughout Ethiopia's major cropping seasons in 2007 and 2008 to determine the degree of genotype-environment interaction and stability analysis. The study followed a rbd design with four replications. The researchers used GGE bi-plots, AMMI, and Combined Analysis of Variance to assess genotype-environment interaction and yield stability. The combined ANOVA revealed significant ($p<0.01$) differences in grain yield across settings, genotypes, and genotype-environment interaction effects. In five of the sixteen environments examined, genotypes EH02-036-2 and Coll.026/01-4 were ranked first.

Sabaghpour *et al.* (2012) assessed for large scale varietal trial for 17 genotypes of autumn chickpeas over a period of three years and five locations in Iran. To comprehend the GEI pattern & AMMI model were employed. FLIP98-126C, FLIP 98-82C, and FLIP 98-201C were shown to be stable genotypes based on a biplot of the first main component and average grain yields for genotypes and locations.

12.3 Comparison of different stability models

Kang *et al.* (1991) used five worldwide yield trials of maize carried out in Louisiana, USA, to compare the efficacy of the rank-sum selection method in yield

with selection-based method. In every trial, the study found a substantial relationship between genotype and environment. Based solely on yield performance, a total of 29 genotypes were chosen. Nevertheless, 32 and 31 genotypes were chosen using the rank-sum technique that included yield and stability parameters (σ^2 and Si_2), of which 11 had lower yields than those chosen only on the basis of yield. This showed that adding stability factors to the selection process resulted in some yield being lost. The authors stressed that when genotype × environment interaction is considerable under a variety of environmental variables, depending only on yield might not be acceptable.

Adugna and Labuschagne (2003) used 2 approaches of nonparametric variables (Si_1 and Si_2) and three parametric measures (CVi, Sv, and Pi) to assess the stability of Linseed genotypes across eighteen settings in Ethiopia. Their analysis revealed that while the cultivar superiority measure (Pi) varied from the other parameters, the coefficient of variability, stability variance, and variance of rankings (Si_2) yielded comparable findings in selecting relatively stable genotypes. Additionally, variance of ranks (Si_2) and stability variance showed a substantial positive correlation according to Spearman Rank Correlation, indicating their efficacy in identifying genetic stability. Additionally, the study found that when evaluating the stability of linseed genotypes, the coefficient of variability outperformed the cultivar superiority measure.

Mangistu *et al.* (2011) examined in order to identify a stable, high-yielding and adaptable genotype for Ethiopia's Western Highlands, sixteen genotypes of field pea over three years (2000–2002) at Shambu and Arjo as well as at Gedo in 2002. To find stable genotypes in a variety of contexts (year-location combinations), they employed regression and AMMI techniques. Bariso, EH92049-1-2-1, and EH92049-2-2 were found to be stable and widely adapted genotypes using both methods, but EH92049-1-3-1 and EH92039-1 were sensitive to environmental changes.

Ashamo *et al.* (2012) have investigated 22 tef genotypes in Southern Ethiopia to determine the best tef genotype based on yield. They used the Additive Main Effect and Multiplicative Interaction (AMMI) approach to quantify genotype and interaction, as well as identify stable genotypes. According to their findings, the AMMI approach outperformed combined regression analysis in dividing G x E variance in small or large data sets (Eberhart and Russell, 1966). DZ-Cr-255 was found to be the most stable tef genotype in their investigation.

Georgieva *et al.* (2015) have employed five field pea (Pisum staivum L.) cultivars from Bulgaria and Ukraine in a small-plot field study conducted between 2012 and 2014. In order to determine stability for different features, they employed the analysis of variance technique, regression analysis in accordance with Eberhart and Russell, Theil approach, Tai approach, and Wricke's ecovalance method. They found that Swit genotype was highly stable and widely adapted. With a score that was closer to zero, Pleven was also found stable genotype among others, meaning that seed yield did not rise as the environmental index did. Glyans was identified as a cultivar with great general adaptability in terms of grain production, 1000 seed weight, and seed weight per plant.

Akcura *et al.* (2009) evaluated the GEI in 20 genotypes of durum wheat using six stability measures, four of which were parametric and two of which were nonparametric. For two years, the genotypes were assessed for grain yield in fourteen settings in Turkey's Central Anatolian Region. A rcbd design with three replications served as the experimental setup. The main effects of genotypes, environments, and GEI were all significant at $p < 0.01$. The durum wheat genotypes' stability was assessed using both parametric (bi, S2 di, Ri 2, Pi) and nonparametric parameter such as (Si (1), Si (2)) univariate stability statistics. Based on six stability metrics, genotypes 20, 13, and 12 were the most stable.

Marcus *et al.* (2009) evaluated eight cassava genotypes in eight locales in the northwest of Paraná State, Brazil, utilizing yield and storage root dry matter content data to compare various phenotypic stability techniques. Although each approach has its own unique characteristics, it was demonstrated that all of the methods used could investigate the stability of cassava genotypes. When the G x E interaction had less of an impact, the approaches of Eskridge, Annicchiarico, Lin, and Binns were the most suitable. When it came to describing particular adaptations of cassava genotypes to favorable and unfavorable situations, the Toler and Burrows technique and the AMMI analysis were the most precise. The most promising genotype was clone IAC 190-89.

Zeki *et al.* (2010) have employed analysis of large scale varietal trial of crops to determine high-yield and stable barley (Hordeum vulgare L.) cultivars in 11 locations between 2001 and 2003 in Turkey's central Black Sea region, as well as to evaluate the link between parametric and nonparametric metrics.

There were notable variations in grain yield amongst barley varieties. This approach suggested Balkan 96 and Erginel as unstable genotypes among others and Fahrettinbey and Sladoran as stable among others.

13. Material and Methods

Genotype × Environment interaction is the deviation from the additive effects of genotype and environment which indicates that the genotype's performance is not consistent across environments. This interaction effect, therefore, poses a challenge in the search for a more stable and high-yielding genotype, which calls for the evaluation of genotypes in different environments through multi-location trial. This chapter focuses on the analysis of genotype × environment interaction using a combination of univariate, multivariate and regression approaches as well as the effect of fixed and random effect models for stability analysis.

13.1 Test environments

Large scale varietal trial (LSVT) on irrigated chickpea genotypes conducted during rabi season of the year of 2024-25 for the present study and test locations were Junagadh, Navsari, SK Nagar, Derol, Dhari and Targhadia of state of Gujarat. The information of different locations indicated that the locations were diverse in soil type, rainfall pattern and also in weather parameters.

13.2 Test materials

Ten genotypes viz. GJG 1907, GJG 2007, GJG 2113, GJG 2115, GJG 2202, GJG 2208, GJG 2210, GJG 2211, GJG 2212, GJG 2213 of irrigated chickpea crop at six multi location along with 6 checks i.e. DY, GG 1, GG 5, NBeG 47, PV, JG 24.

The experiment used randomized block design (RBD) design with four replication for all the trials in different location. The Net plot size was 4.0m × 3.0m for every environment under study. Data on seed yield (kg/plot) of irrigated chick pea genotypes grown at different test location is gathered and subjected to stability analysis by different approaches as given under.

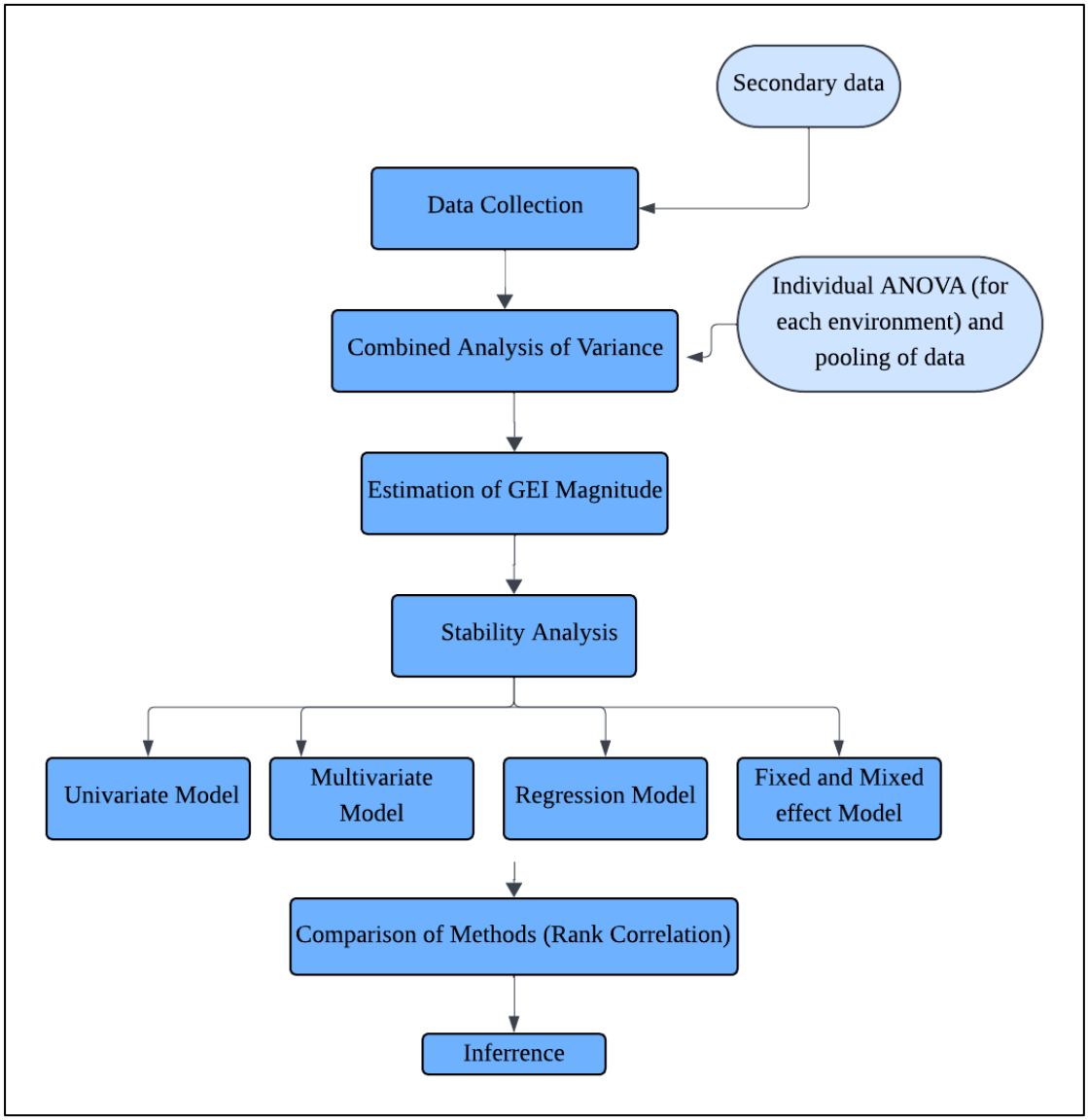

Figure 1: Methodology framework

14. Statistical Analysis

14.1 Methods of analysis employed for data on multi-location trial on chickpea genotypes

The seed yield data were subjected to statistical analysis using various methods of stability analysis via different univariate, multivariate and regression approach. We will also check the effect of fixed effect (AMMI Model) and random effect model (BLUP model).

The most popular technique for determining if genotype × environment interaction (GEI) exists in the replicated trials is a combined analysis of variance procedure. The stable genotype or genotypes can be identified using several techniques

if GEI is determined to be substantial. The current study on chickpeas used the following techniques.

14.1.1 Analysis of Variance

Analysis of variance of large scale varietal trial is useful for evaluating variance components related to different sources of variation. The following Randomized Block Design model was used to analyze the MLT data both individually and collectively (Panse and Sukhatme, 1967). Analysis of variance as the traditional methodology for examining the overall yield variation found in GEI observations (Fisher, 1918). The mistake in predicting the genotype means caused by variations in soil fertility and other factors such as shading and competition between plots, is measured by the within-environment residual mean square. After removing the replicate effect from the combined data, the GE observations are separated into two sources: (a) non-additive effects resulting from GEI and (b) additive main impact for genotypes and environments. The observed (Yij) mean yield of the ith genotype in the jth environment can be expressed as follows using the anova of the combined data:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \varepsilon_{ij} \qquad \textbf{...Eq. 14.1}$$

Where, μ = General mean effect

α_i = Effect due to i[th] genotype,

β_j = Effect due to j[th] environment,

$\alpha\beta_{ij}$ = Effect due to i[th] genotype and j[th] environment,

ε_{ij} = Random error corresponding to i[th] genotype and j[th] environment

Table 1: ANOVA Table for Combined Analysis

Source of Variaition	DF	SS	MSS	F
$Location$	$k-1$	SSK	MSK	
$Block\ within\ location$	$k(r-1)$	SSB	MSB	
$Treatment$	$t-1$	SST	MST	$F1$
$Interaction$	$(k-1)(t-1)$	$SS(KxT)$	$MS(KxT)$	$F2$
$Pooled\ Error$	$k(r-1)(t-1)$	SSE	MSE	
$Total$	$krt-1$	TSS		

14.1.2 STABILITY ANALYSIS

The overall summary of genotype response patterns to environmental change is provided by stability analysis. There are techniques for estimating genotype stability based on the GEI. For analysis of stability we use different parametric & non parametric stability measures by using R studio software. To analyze the GEI effect in plant breeding experiments, Olivoto and Lucio created the R package "metan." Breeders may estimate several statistical approach and construct the AMMI model and GGE biplot with this software. The major significant and widely applied approaches are covered in the sections as follow.

14.1.2.1 Francis and Kannenberg's Coefficient of Variability (CV_i)

He proposed a parametric stability statistic known as coefficient of variation which was based on standard deviation, mean yield and environmental variance

$$CV = \frac{\sigma_{x_i}}{\bar{x}_i} \times 100 \qquad \textbf{...Eq. 14.2}$$

Where,

σ_x = S.D of a genotype means across environments

$\bar{x}$ = Grand mean

The genotype with low environmental variance, low CV, and high mean yield is considered as most desirable genotype. Test genotype can be classified into four categories. According to mean yield and CV values, if we compare mean yield and CV by plotting them x and y axis respectively, group 1 consist high yield and little variance, group 2 consist high yield and significant variance, group 3 comprises low yield and low variance while group 4 consists low yield and significant variance.

14.1.2.2 Lin and Binns Superiority (P_i)

Lin and Binns (1988) have proposed a superiority measure which was based on the distance mean square between the cultivar's response and the maximum response over locations and it is also known as "cultivar general superiority". It is denoted by P_i and defined as

$$P_i = \sum_{i=j-1}^{q} (X_{ij} - M_{.j})^2 / 2q \qquad \textbf{...Eq. 14.4}$$

Where,

P_i = Superiority measure,

X_{ij} = Yield of the i^{th} genotype grown in the j^{th} environment,

$M_{.j}$ = Maximum yield in the j^{th} environment.

14.1.2.3 Wricke's Ecovalence (W_i)

Ecovalence may be defined as the interaction of the ith genotype with its environments, squared and summed across environments. It was proposed by Wricke in 1962 and 1964. He suggested that GEI sum of square require each genotype's contribution. It is denoted by W_i and defined as

$$W_i = (Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})^2 \quad \textbf{…Eq. 14.5}$$

Where,

Y_{ij} = Mean performance of i^{th} genotype in the j^{th} environment

$Y_{i.}$ and $Y_{.j}$ = Genotype and environment mean deviations, respectively

$Y_{..}$ = Overall mean.

The genotypes with low W_i values are more stable since they have smaller variances from the mean across contexts.

14.1.2.4 Shukla's Stability Variance (σ_i^2)

Shukla (1972) introduced stability variance, a modified version of ecovalence that provides an unbiased estimate of the GE variance for each genotype.

$$\sigma_i^2 = \frac{g}{(g-2)(e-2)} \sum_{j-1}^{q} (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2 - \sum_{i}^{p} \sum_{j}^{q} (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2$$

…Eq. 14.6

Where, σ_i^2 = Stability variance

X_{ij} = Mean yield of the i^{th} genotype in the j^{th} environment,

$\bar{X}_{i.} = Mean\ of\ the\ genotype$ i^{th} in all environments,

$\bar{X}_{.j} = Mean$ of all genotypes in j^{th} environments,

$\bar{X}_{..}$ = Overall mean of genotypes in all environments.

14.1.2.5 Annicchiarico's Genotypic Confidence Index (Wi_g)

Annicchiarico's Genotypic Confidence Index (Wi_g) is used for stability analysis in plant breeding. It quantifies the confidence in genotype performance across different environments.

$$Wi_g = \frac{\text{Genotypic variance}}{\text{Genotypic variance} + \frac{\text{Residual variance}}{\text{Number of replications}}} \quad \textbf{…Eq. 14.7}$$

Where,

Genotypic variance = Variability due to genetic differences among genotypes

Residual variance = Accounts for environmental variation

Number of replications = Number of times each genotype is tested across environments

14.1.3 Regression approach

14.1.3.1 Eberhart and Russell model

In 1966, he s suggested the following model

$$Y_{ij} = \mu_i + b_i I_J + \delta_{ij} \qquad \textbf{...Eq. 14.8}$$

Where,

Y_{ij} = Mean response of ith genotype in jth environment

μ_i = the genotype mean over all environments

bi = Regression coefficient of the i^{th} genotypes on environmental means

I_J = the environmental index calculated as $I_J = Y_{.J} - Y..$

δ_{ij} = deviation of i^{th} in j^{th} environment from regression

Table 2: ANOVA for Eberhart and Russell model

Source of Variaition	DF	DF	MSS	F
Genotypes	$g-1$	$k-1$	MS1	MS1/MS3
Environments + G × E	$g(e-1)$	$k(r-1)$		
Environment(linear)	1	$t-1$		
G × E (linear)	$(g-1)$	$(k-1)(t-1)$	MS2	MS2/MS3
Pooled deviation	$g(e-2)$	$k(r-1)(t-1)$	MS3	MS3/MS4
Genotype 1	e-2	$krt-1$		
Genotype 2	e-2			
……				
…….				
Genotype n	e-2			
Pooled error	e(r-1)(g-1)			

14.1.4: Multivariate Analysis Methods

Multivariate analysis has three primary works (i) To remove data noise (ii) To provide an overview of the data and (iii) To determine the data's structure. Crossa (1990) Multivariate analysis's primary goal is to explain the data's internal structure so that hypotheses can be developed and subsequently validated using statistical techniques (Gauch, 1982a & b).

This technique is also suitable for analyzing two-way matrices of genotypes G and E environments. Any genotype's response in E environment can be

recognized by the pattern of E dimensional space. Where the one coordinate belongs to yield or another metric of the genotype in a particular environment

14.1.4.1 Principal Component Analysis (PCA)

Karl Pearson proposed Principal component analysis (PCA) in 1901, which is the most popular multivariate technique and is used for dimension reduction. Its goal is to transform the data into smaller one which still contains most of the information in the data.

Principle component analysis (PCA), a generalization of linear regression that provides multiple statistics and the scores on the principal component axes are used to characterize a genotype's response.

14.1.4.2: Additive Main Effects and Multiplicative Interaction (AMMI)

The method which combines both principal components analysis and analysis of variance into a single unified methodology is known as additive main effect and multiplicative interaction (AMMI) method (Gauch, 1988). It is useful to analyze multi locational trials. The three main purpose of AMMI technique is (i) model diagnostic, (ii) clarifies GEI and (iii) to improve the accuracy of yield estimates

The principal components analysis of the genotype-environment interaction is combined with the analysis of variance for the main effects of both genotype and environment in the AMMI model. It has shown to be helpful in comprehending complicated GEI. A helpful bi plot that displays the main and interaction effects for both the genotypes and environments may be created by graphing the results .

AMMI model that combines analysis of variance (ANOVA) into a single model with multiplicative and additive parameters is

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij} \qquad \textbf{...Eq. 14.9}$$

Where,

Y_{ij} = Yield of the i^{th} genotype in the j^{th} environment ,

μ = Grand mean ,

G_i = Genotype deviations from the grand mean ,

E_j = Environment deviations from the grand mean ,

λ_k = Eigenvalue of the PCA analysis axis k ,

α_{ik} = Genotype principal component scores for axis k ,

γ_{jk} = Environment principal component scores for axis k ,

n = Number of principal components retained in the model ,

e_{ij} = Error term .

The AMMI model, which combines principal component analysis and variance analysis, will help you better understand GEI and get more accurate yield estimates . A bi-plot is a graphical representation that explains the interaction by plotting PCA scores against one another and allowing for visual inspection and comprehension of the GEI components. By integrating genotypic stability data and biplot display, genotypes can be classed based on how similar they perform in different environments.

14.1.4.3: The AMMI Stability Value (ASV)

It was introduced by Purchase in 1997. The yield stability indicates that a quantitative stability measure is necessary to rank and quantify genotype, however the AMMI model does not include this clause. Distance in ASV, which is measured from zero and is determined in terms of a two-dimensional scatter graph of IPCA 1 scores against to IPCA 2 scores. The total G x E sum of square, which is weighted by the proportion that differs between the IPCA 1 and IPCA 2 scores, is used to compensation the relative contributions of the two scores.

"AMMI Stability Value (ASV)"= $\sqrt{[\frac{IPCA1\ Sum\ of\ Square}{IPCA2\ Sum\ of\ Square}(IPCA1\ score)]}$ **…Eq. 14.10**

Since ASV is the distance starting from zero and determined in terms of a two-dimensional scatter graph of IPCA 1 scores against to IPCA 2 scores. IPCA I score contributes more to G x E sum of square. The distance from zero can be determined by Pythagoras Theorem.

14.1.4.4: AMMI Based Stability Parameter (ASTAB)

Rao and Prabhakaran introduced the AMMI-based stability parameter (ASTAB) as follows:

$$ASTAB = \sum_{n=1}^{N} \lambda_n {\gamma_{in}}^2 \qquad \textbf{…Eq. 14.11}$$

Where, λ_n and γ_{in} are the eigenvalue of the n^{th} IPCA and the eigenvector value for the i^{th} genotype. A genotype is considered to be more stable when the value of this statistic is lower.

14.1.4.5: Modified AMMI Stability Value (MASV)

The modified AMMI stability values (MASV) (Zali *et al.,* 2012) is another stability statistic and it is given as

$$\text{MASV} = \sqrt{\sum_{n=1}^{N-2}((\frac{\text{SSIPCA}_n}{\text{SSIPCA}_{n+1}})(\text{IPCA}_n)^2 + (\text{IPCA}_N)^2} \qquad \textbf{…Eq. 14.12}$$

Using all relevant IPCAs in the MASV statistic is the primary distinction between ASV and MASV. Like ASV, the most stable genotype will be determined by taking the lowest MASV value.

14.1.4.6: Annicchiarico's D Parameter values (Da)

The stability parameter according to the Annicchiarico's (1997) method is given by Equation 13.13:

$$D_a = \sqrt{\sum_{n=1}^{N'}(\lambda_n \gamma_{in})^2} \quad \textbf{...Eq. 14.13}$$

Where,

N' = Number of significant interaction principal component axis (IPCs) that were retained in the AMMI model via F tests

λ_n = The singular value for the IPC

γ_{in} = The eigenvector value for ith genotype

14.1.4.7: Zhang's D Parameter (Dz)

The stability parameter according to the Zhang *et al.* (1998) method is given by Equation 13.14:

$$D_z = \sqrt{\sum_{n=1}^{N'} {\gamma_{in}}^2} \quad \textbf{...Eq. 14.14}$$

Where,

N' = Number of significant interaction principal component axis (IPCs) that were retained in the AMMI model via F tests

γ_{in} = The eigenvector value for ith genotype

14.1.4.8: Sums of the Averages of the Squared Eigenvector Values (EV)

The stability parameter according to the Zobel (1994) method is given by Equation 13.15:

$$EV = \sum_{n=1}^{N'} \frac{{\gamma_{in}}^2}{N'} \quad \textbf{...Eq. 14.15}$$

Where,

N' = Number of significant interaction principal component axis (IPCs) that were retained in the AMMI model via F tests

γ_{in} = The eigenvector value for ith genotype

14.1.4.9: Stability Measure Based on Fitted AMMI Model (FA)

The stability parameter according to the Raju (2002) method is given by Equation

$$FA = \sum_{n=1}^{N'} {\lambda_n}^2 {\gamma_{in}}^2 \quad \textbf{...Eq. 14.16}$$

Where,

N' = Number of significant interaction principal component axis (IPCs) that were retained in the AMMI model via F tests

γ_{in} = The eigenvector value for i[th] genotype

${\lambda_n}^2$ = Eigenvalue the corresponding the value of λ_n

14.1.4.10: AMMI Stability Index (ASI)

It is also used to measure stability and it is proposed by Jambhulkar *et al.* The lowest value of this statistic (ASI) shows the most stability. ASI can be measured as

$$\text{ASI} = \sqrt{[(\text{IPCA1} \times {\theta_1}^2)^2 + (\text{IPCA2} \times {\theta_2}^2)^2]} \quad \textbf{...Eq. 14.17}$$

Where,

IPCA1 and IPCA2= scores of the two first principal component interactions

${\theta_1}^2$= Percentage sum of squares explained by the first IPCA effects.

${\theta_2}^2$= Percentage sum of squares explained by the second IPCA effect.

14.1.4.11: Modified AMMI Stability Index (MASI)

It was proposed by Ajay *et al.* (2019) and it is given as

$$MASI = \sqrt{\sum_{n=1}^{N} {IPCA_n}^2 \times {\theta_n}^2} \quad \textbf{...Eq. 14.18}$$

Where, $IPCA_n$ and ${\theta_n}^2$ are the scores of the n[th] IPCA and the percentage sum of square explained by the n[th] IPCAs effects, respectively. The lowest value of this statistic shows the most stability.

14.1.4.12: Modified Stability Value (MASV)

The modified AMMI stability value (MASV) was suggested as stability statistic by Zali *et al.* as follows:

$$\text{MASV} = \sqrt{\sum_{n=1}^{N-2} (\frac{SSIPCA_n}{SSIPCA_{n+1}})(IPCA_n))^2 + (IPCA_N)^2} \quad \textbf{...Eq. 14.19}$$

Where,

$SSIPCA_1$ = S.S of the 1[st] IPC

$SSIPCA_2$ = S.S of the 2[nd] IPC

$SSIPCA_n$ = S.S of the n[th] IPC

14.1.4.13: Sums of the Absolute Value of the IPC Scores (SIPC)

The stability parameter according to the Sneller *et al.* (1997) method is given by Equation

$$SIPC = \sum_{n=1}^{N} |\lambda_n{}^{0.5} \gamma_{in|} \quad \textbf{…Eq. 14.20}$$

Where,

λ_n = The singular value for the IPC

γ_{in} = The eigenvector value for i[th] genotype

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14.1.5: Best Linear Unbiased Prediction (BLUP) Based Stability Statistics

BLUP is used for the estimation of random effects in the linear model. There are several parameters for measuring stability which are based on BLUP and the restricted maximum likelihood (REML).

14.1.5.1: Harmonic Mean of Genotypic Values (HMGV)

The first parameter is the harmonic mean of genotypic values (HMGV), which defines the most stable genotype as the one with the highest harmonic mean across environments :

$$HMGV = \frac{E}{\sum_{j=1}^{E} \frac{1}{GV_{ij}}} \quad \textbf{…Eq. 13.21}$$

Where, GV_{ij} = Genotypic values (BLUP) for the i[th] genotype in the j[th] environment ,

E = Number of environments

14.15.2: Relative Performance of Genotypic Values (RPGV)

The relative performance of genotypic values (RPGV), which is calculated as follows and is regarded as an adaptability index, is the second parameter .

$$RPGV = \frac{1}{E} \sum_{j=1}^{E} GV_{ij}/\mu_j \quad \textbf{…Eq. 14.22}$$

Where,

GV_{ij} = Genotypic values (BLUP) for the i[th] genotype in the j[th] environment ,

E = Number of environments

μ_j = Grand mean of each environment j.

14.1.5.3: Harmonic Mean of RPGV (HMRPGV)

The third BLUP-based stability metric that takes stability, adaptability, and mean performance into account at the same time is the Harmonic mean of RPGV (HMRPGV). The following formula is used to determine this parameter :

$$HMRPGV = \frac{E}{\sum_{j=1}^{E} \frac{1}{GV_{ij}/\mu_j}} \quad \textbf{...Eq. 14.23}$$

Where, GV_{ij} = Genotypic values (BLUP) for the i[th] genotype in the j[th] environment,

E = Number of environments

μ_j = Grand mean of each environment j.

14.1.6 Non-parametric test

14.1.6.1 Nassar and Huhn

Huhn presented a non-parametric stability statistics in 1979 for multi environment trial. There are four rank-based statistics which are used for

1. Statistics S1 shows the average of a genotype's absolute rank differences across all tested contexts.

$$S1 = 2\sum_{j}^{p-1} \frac{\sum_{j'=j+1}^{p} |r_{ij} - r_{ij}'|}{[P(P-1)]} \quad \textbf{...Eq. 14.24}$$

2. S2, which represents the variance between the ranks across all tested situations.

$$S2 = \frac{\sum_{j=1}^{p} (r_{ij} - \bar{r}_{i.})^2}{(P-1)} \quad \textbf{...Eq. 14.25}$$

3. S3 provides the total of each genotype's absolute departures from the rank mean.

$$S3 = \frac{\sum_{j=1}^{p} (r_{ij} - \bar{r}_{i.})^2}{\bar{r}_{i.}} \quad \textbf{...Eq. 14.26}$$

4. Statistics S6 shows the sum of squares of rank for each genotype in relation to the mean of rankings.

$$S6 = \frac{\sum_{j=1}^{p} |r_{ij} - \bar{r}_{i.}|}{\bar{r}_{i.}} \quad \textbf{...Eq. 14.27}$$

Where

r_{ij} = Rank of the ith genotype in jth environment ,

$\bar{r}_{i.}$ = Mean rank across all environments for each genotype

14.1.6.2.8: Thennarasu's Statistics

Based on ranks of adjusted means of the genotypes in each environment, Thennarasu (1995) suggested an another set of nonparametric statistics (NPi(1), NPi(2), NPi(3) and NPi(4)). Stable genotypes were defined as those whose position remained unchanged in relation to the others in the set of environments evaluated. These were computed in the manner described below:

$$NP_i^{(1)} = \frac{1}{P}\sum_{j=1}^{p} |r_{ij}{}^{*} - M_{di}{}^{*}| \qquad \textbf{…Eq. 14.28}$$

$$NP_i^{(2)} = \frac{1}{P}\sum_{j=1}^{p} \frac{|r_{ij}{}^{*} - M_{di}{}^{*}|}{M_{di}} \qquad \textbf{…Eq. 14.29}$$

$$\mathrm{NP_i^{(3)}} = \frac{\sqrt{\sum(\mathrm{r_{ij}}^{*} - \bar{\mathrm{r}}_{\mathrm{i.}}{}^{*})^2/\mathrm{P}}}{\bar{\mathrm{r}}_{\mathrm{i.}}} \qquad \textbf{…Eq. 14.30}$$

$$\mathrm{NP_i^{(4)}} = \frac{2}{\mathrm{P(P-1)}}\left[\sum_{\mathrm{j=1}}^{\mathrm{p-1}}\sum_{\mathrm{j^1=j+1}}^{\mathrm{p}} \frac{|\mathrm{r_{ij}}^{*} - \mathrm{r_{ij^1}}^{*}|}{\bar{\mathrm{r}}_{\mathrm{i.}}}\right. \qquad \textbf{…Eq. 14.31}$$

Where

the $r_{ij}{}^{*}$ is the rank of ith genotype in the jth environment based on adjusted data ,

$M_{di}{}^{*}$ is the median ranks for adjusted data ,

$\bar{\mathrm{r}}_{\mathrm{i.}}$ and M_{di} are the same parameters obtained from the original data (unadjusted)

- Higher stability is indicated by low values in these statistics.

14.1.7: Spearman's Rank Correlation

Spearman's coefficient of rank correlation (rs) was calculated in order to statistically compare the previously discussed stability analysis methods (Steel and Torrie, 1980). Let us consider n genotypes are arranged in some order of magnitude of two stability parameters then

$$d_i = X_i - Y_i \ (i=1,2,3,4\ldots\ldots n) \qquad \textbf{…Eq. 14.32}$$

Where,

X_i = Ranking order (or number) of the i^{th} genotype for the first parameter,

Y_i = Ranking order of the i^{th} genotype for the second parameter.

Spearman's rank correlation coefficient (r_s) can be described as:

$$r = 1 - \frac{6\sum {d_i}^2}{n(n^2-1)} \qquad \textbf{…Eq. 14.33}$$

The significance of r was tested by means of Student's t test (Steel and Torrie, 1980) where:

$$t = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}} \sim t_{n-2} \qquad \textbf{…Eq. 14.34}$$

If $t \geq t_{(\alpha: n-2)}$, r is deemed to be extremely significant, and the null hypothesis is rejected. Spearman Coefficient of rank correlation was determined for the comparison between the above stability analysis procedures. In the following order two stability parameter i.e. X_i and Y_i. It displays the genotypes' ranking order.

14. References

Akcura and Kaya. (2008) Nonparametric stability methods for interpreting genotype by environment interaction of bread wheat genotypes (*Triticum aestivum* L.). *Genetics and Molecular Biology*, **31(4)**: 906-913.

Akcura, Kaya, and Seyfi. (2009) Evaluation of durum wheat genotypes using parametric and nonparametric stability statistics. *Turkish Journal of Field Crops,* **14**(2):111-122.

Ashamo, M. and Belay, G. (2012). Genotype x environment interaction analysis of tef grown in southern Ethiopia using additive main effects and multiplicative interaction model. *Journal of Biology, Agriculture and Healthcare*, ***2***(1), pp. 66-72.

Chaithra, H. R. (2016). Comparison of Parametric and Non Parametric Stability Models for Yield ff Finger Millet, *(Eleusine coracana(L.) Gaertn.)* Genotypes, M.Sc. Thesis, University of Agricultural Sciences, Bengaluru.

Deka, S.D. and Talukdar, P. (1997). Stability behaviour of same soybean (*Glycine max*. (L.) Merrill) genotype under environments variability. *Indian J. Genet*. **57**(1):36-39.

Francis, T. R. and Kannenburg, L. W. (1978). Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. *Can. J. Plant Sci.* **58**: 1029-1034.

Gabriel, K. R. (1971). The biplot graphic display of matrices with application to principal component analysis. *Biometrika* **58**(3): 453-467.

Genotypes (*Oryza Sativa* L.). *Journal of Rice Research,* **5**(1): 17-25.

Georgieva, N., Nikolova, I. and Kosev, V. (2015). Adaptation and stability of field peas (*Pisum sativum* L.) cultivars. J. *Global Agriculture and Ecology*, **3(1)**, pp. 1-10.

Goa, Y. and Mohammed, H. (2013). Genotype x environment interaction and yield stability in Field pea (*Pisum sativum* L.) tested over different locations in Southern Ethiopia. *Journal of Biology, Agriculture and Healthcare*, ***3*(19)**, pp. 91-100.

Hanson, W. D. (1970). Genotypic stability. *Theor. Appl. Genet.* **40**: 226-231.

Huehn, M. 1990. Non-parametric measures of phenotypic stability II. Application. *Euphytica* **47**: 195-201.

Joshi, H. J, J.J. Vaghani, B.V. Radadia, and D.R. Mehta (2005). Genotype x environment interaction and stability analysis in soybean. *Adv.Pl.Sci.* **18**(2): 515-518

Lodhi, R., Prasad, L. C., Madakemohekar, A. H., Bornare, S. and Prasad, R. (2015). Study of Genetic parameters for yield and yield contributing trait of elite genotypes of barley (*Hordeum vulgare* L.). *Indian Research Journal of Genetics and Biotechnology, **7*****(1),*** pp. 17-21.

Kabir, M. R., Hossain, A., Rahman, M. M., Hakim, M. A. and Sarker, M. A. Z. (2009). Stability analysis of wheat for grain yield affected by different environment. *Bangladesh Research Publication Journal*, ***3***, pp. 833-840.

Kang, M. S. Gorman, D. P. and Pham, H. N. (1991). Application of a stability statistic to international maize yield trials. *Theoretical and Applied Genet.* **18(2)**: 162-165.

Mangistu, G., Dhaba, C., Temesgen, A., Lule, D. and Geleta, N. (2011). Genotype x environment interaction for yield in field pea (*Pisum sativum* L.*). East African Journal of Sciences, **5*****(1)***, pp. 6-11.

Marcus Vinicius Kvitschal., Pedro Soares Vidigal Filho., Carlos Alberto Scapim Maria., Edvaldo Sagrilo., Manoel Genildo Pequeno., and Fabricio Rimoldi. (2009). Comparison of Methods for Phenotypic Stability Analysis of Cassava (*Manihot esculenta Crantz*) Genotypes for Yield and Storage Root Dry Matter content. *Brazilian archives of biology and technology*, **52(1)**: 163-175.

Martins, L. F., Carvalho and M. F. de (2006). Use of nonparametric selection indexes in studies of adaptability and stability of oat cultivars. *Crop Breeding and Applied Biotechnology*, 6: 95–103.

Mohammadi, M., Karimizadeh, R., Hosseinpour, T., Kalateharabi, M., Khanzadeh, H., Sabaghnia, N., Mohammadi, P. and Hasanpour, H. M. (2012). Analysis of genotype, environment and genotype x environment interaction in bread wheat in warm rainfed areas of Iran. *Crop Breeding Journal, **2***(1), pp. 63-70.

Mishra, D.K., G.P. Mishra, M.S. Baghel (1999). Genotype x Environment interaction for grain yield its component in soybean. *Ann. Agric. Res*. **20**(1): 56-59.

Nabi T. (2023) Comparison of Parametric and Non-Parametric Statistical Methods for Stability Analysis, M.Sc. Thesis, Division of Agricultural Statistics, University of Agricultural Sciences and Technology of Kashmir.

Nassar, R. and Huehn, M. (1987). Studies on estimation of phenotypic stability: Tests of significance for non-parametric measures of phenotypic stability. *Biometrics* **43**: 45-53.

Parmar, D. J., Patel, J. S., Mehta, A. M., Makwana, M. G., and Patel, S. R. (2012). Non-parametric methods for interpreting genotype × environment interaction of rice genotypes (*Oryza sativa* L.). *Journal of Rice Research*, **5**(1–2), 17–23.

Parmar, D, K. (2010), Stability analysis for growth and yield attributes in soybean (*Glycine max* (L.) Merrill.), Department of Plant Breeding & Genetics, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya

Rawat, G.S., Nandan Mehta, Y. Mishra and R.S. Shukla (2001). Phenotypic stability for seed quality characters in soybean. *JNKVV Res. J*. **34**(1/2): 65-66.

Roy, S.B. and Roquib, M.A. (1998). Varietal adaptation of soybean (*Glycine max*. (L.) Merrill). *Ann. Agric. Res*. **32(2)**: 145-46.

Sabaghpour, S.H., Razavi, F., Danyali, S.F., Tobe, D., and Ebadi, A. (2012). Additive Main Effect and Multiplicative Interaction Analysis for Grain Yield of Chickpea (*Cicer arietinum* L.) in Iran. *International Scholarly Research Network (ISRN) Agronomy,* **639381**:1-6.

Shukla, G. K. (1972). Some statistical aspects of partitioning genotype environmental components of variability. *Heredity* **29**: 237-245.

Singh, R.K. and choudary, B.D. (1984). *Biometrical methods in quantitative genetic analysis*. Pub. Kalyani. Ludhiana.

Tolessa, T. T., Keneni, G., Sefera, T., Jarso, M. and Bekele, Y. (2013). Genotype x environment interaction and performance stability for grain yield in field pea (*Pisum sativum* L.) genotypes. *International Journal of plant breeding, 7*(2), pp. 116-123.

Vieira, E. A., Carvalho, F. I. F., Oliveira, A. C., Benin, G., Lorencetti, C., Zimmer, P. D., Floss, E. L., and Figuerola, A. Comparison of parametric and non-parametric stability models for yield of finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes

Wricke, G. (1962). Über eine Methode zur Erfassung der ekologischen Streubreite in Feldversuchen Z. *Pflanzenzücht* **47**: 92-96.

Yadav, A. (2024). Study on Various Statistical Methods for Genotype X Environment Interaction and Yield Stability ff Fieldpea Genotypes, M.Sc. Thesis, Department of Statistics and Computer Science, Banda University of Agriculture & Technology.

Yates, F. and Cochran, W. G. (1938). The analysis of groups of experiments. *J. Agric. Sci.* **28**: 556-580.

Zeki Mut., Nevzat Aydin., Bayramoglu, H.O., and Hasan Ozcan. (2009), Interpreting Genotype × Environment Interaction in Bread Wheat (*triticum aestivum* L.) Genotypes using Nonparametric Measures. *Turk J Agric.,* **33**: 127-137.